P0#8 (handwritten)

PCT09

RAW SEQUENCE LISTING   DATE: 07/15/2001
PATENT APPLICATION: US/09/744,085   TIME: 20:07:33

Input Set : **A:\744085seq.jun.txt**
Output Set: **N:\CRF3\07152001\I744085.raw**

ENTERED

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 3 <110> APPLICANT: Schaffer, Arthur
 4        Levin, Ilan
 5        Petreikov, Marina
 6        Bar, Moshe
 8 <120> TITLE OF INVENTION: Controlling Starch Synthesis
10 <130> FILE REFERENCE: U-013220-5
12 <140> CURRENT APPLICATION NUMBER: US 09/744,085
C--> 13 <141> CURRENT FILING DATE: 2001-06-21
15 <150> PRIOR APPLICATION NUMBER: PCT/IL99/00396
16 <151> PRIOR FILING DATE: 1999-07-19
18 <150> PRIOR APPLICATION NUMBER: IL 125425
19 <151> PRIOR FILING DATE: 1998-07-20
21 <160> NUMBER OF SEQ ID NOS: 10
23 <170> SOFTWARE: PatentIn Ver. 2.1
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26 <211> LENGTH: 23
27 <212> TYPE: DNA
28 <213> ORGANISM: Lycopersicon hirsutum
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71 <211> LENGTH: 22
72 <212> TYPE: DNA
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 80 <211> LENGTH: 23
 81 <212> TYPE: DNA
 82 <213> ORGANISM: Lycopersicon hirsutum
 84 <400> SEQUENCE: 7
 85 tttcgtcttc tcatctcgcc gga                                     23
 88 <210> SEQ ID NO: 8
 89 <211> LENGTH: 23
 90 <212> TYPE: DNA
 91 <213> ORGANISM: Lycopersicon hirsutum
 93 <400> SEQUENCE: 8
 94 ggcgatttag agaggcagag ttg                                     23
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 98 <211> LENGTH: 1563
 99 <212> TYPE: DNA
100 <213> ORGANISM: Lycopersicon hirsutum
102 <220> FEATURE:
103 <221> NAME/KEY: CDS
104 <222> LOCATION: (1)..(1563)
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109  1               5                  10                  15
111 aat gga gag aag gag att ttt ggg gag aag atg aga ggg agt ttg aac   96
112 Asn Gly Glu Lys Glu Ile Phe Gly Glu Lys Met Arg Gly Ser Leu Asn
113              20                  25                  30
115 aac aat ctc agg att aat cag ttg tcg aaa agt ttg aaa ctt gag aag  144
116 Asn Asn Leu Arg Ile Asn Gln Leu Ser Lys Ser Leu Lys Leu Glu Lys
117          35                  40                  45
119 aag gag aag aag att aaa cct ggg gtt gct tac tct gtg atc act act  192
120 Lys Glu Lys Lys Ile Lys Pro Gly Val Ala Tyr Ser Val Ile Thr Thr
121      50                  55                  60
123 gaa aat gac aca gag act gtg ttc gta gat atg cca cgt ctt gag aga  240
124 Glu Asn Asp Thr Glu Thr Val Phe Val Asp Met Pro Arg Leu Glu Arg
125  65                  70                  75                  80
127 cgc cgg gca aat ccc aag gat gtg gct gca gtc ata tta gga gga ggc  288
128 Arg Arg Ala Asn Pro Lys Asp Val Ala Ala Val Ile Leu Gly Gly Gly
129                  85                  90                  95
131 gaa ggg acc aag tta ttc cca ctt aca agt aga act gca acc cct gct  336
132 Glu Gly Thr Lys Leu Phe Pro Leu Thr Ser Arg Thr Ala Thr Pro Ala
133              100                 105                 110
135 gtt ccg gtt gga gga tgc tac agg ctc ata gac atc ccg atg agc aac  384
136 Val Pro Val Gly Gly Cys Tyr Arg Leu Ile Asp Ile Pro Met Ser Asn
137          115                 120                 125
139 tgt atc aac agt gct att aac aag att ttt gtg ctg aca cag tac aat  432
140 Cys Ile Asn Ser Ala Ile Asn Lys Ile Phe Val Leu Thr Gln Tyr Asn
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143 tct gct gcc ctg aat cgt cac att gct cga acg tat ttt ggc aat ggt      480
144 Ser Ala Ala Leu Asn Arg His Ile Ala Arg Thr Tyr Phe Gly Asn Gly
145 145               150                  155                  160
147 gtg agc ttt gga gat gga ttt gtc gag gta cta gct gca act cag aca      528
148 Val Ser Phe Gly Asp Gly Phe Val Glu Val Leu Ala Ala Thr Gln Thr
149               165                  170                  175
151 cct ggg gaa gca gga aaa aaa tgg ttt caa gga aca gca gat gct gtc      576
152 Pro Gly Glu Ala Gly Lys Lys Trp Phe Gln Gly Thr Ala Asp Ala Val
153               180                  185                  190
155 aga aaa ttt ata tgg gtt ttt gag gac gct aag aac aag aat att gaa      624
156 Arg Lys Phe Ile Trp Val Phe Glu Asp Ala Lys Asn Lys Asn Ile Glu
157           195                  200                  205
159 aat atc ctt gta tta tct ggg gat cat ctt tat agg atg gat tat atg      672
160 Asn Ile Leu Val Leu Ser Gly Asp His Leu Tyr Arg Met Asp Tyr Met
161      210                  215                  220
163 gag ttg gtg cag aac cat att gac aga aat gct gat att act ctt tca      720
164 Glu Leu Val Gln Asn His Ile Asp Arg Asn Ala Asp Ile Thr Leu Ser
165 225               230                  235                  240
167 tgt gca cca gct gag gac agc cga gca tca gat ttt ggg ctg gtc aag      768
168 Cys Ala Pro Ala Glu Asp Ser Arg Ala Ser Asp Phe Gly Leu Val Lys
169               245                  250                  255
171 att gac agc aga ggc aga gtt gtc cag ttt gct gaa aaa cca aaa ggt      816
172 Ile Asp Ser Arg Gly Arg Val Val Gln Phe Ala Glu Lys Pro Lys Gly
173               260                  265                  270
175 ttt gag ctt aaa gca atg caa gta gat act act ctt gtt gga tta tct      864
176 Phe Glu Leu Lys Ala Met Gln Val Asp Thr Thr Leu Val Gly Leu Ser
177           275                  280                  285
179 cca caa gat gcg aag aaa tcc cct tat att gct tca atg gga gtt tat      912
180 Pro Gln Asp Ala Lys Lys Ser Pro Tyr Ile Ala Ser Met Gly Val Tyr
181      290                  295                  300
183 gtt ttc aag aca gat gta ttg ctg aag ctc ttg aaa tgg agc tac ccc      960
184 Val Phe Lys Thr Asp Val Leu Leu Lys Leu Leu Lys Trp Ser Tyr Pro
185 305               310                  315                  320
187 act tct aat gat ttt ggc tct gaa att ata cca gca gct att gat gat     1008
188 Thr Ser Asn Asp Phe Gly Ser Glu Ile Ile Pro Ala Ala Ile Asp Asp
189               325                  330                  335
191 tac aat gtc caa gca tac att ttc aaa gac tat tgg gag gac att gga     1056
192 Tyr Asn Val Gln Ala Tyr Ile Phe Lys Asp Tyr Trp Glu Asp Ile Gly
193               340                  345                  350
195 aca att aaa tct ttc tat aat gct agc ttg gcg ctc aca caa gag ttt     1104
196 Thr Ile Lys Ser Phe Tyr Asn Ala Ser Leu Ala Leu Thr Gln Glu Phe
197           355                  360                  365
199 cca gag ttc caa ttt tat gat cca aaa aca cct ttt tac aca tct cct     1152
200 Pro Glu Phe Gln Phe Tyr Asp Pro Lys Thr Pro Phe Tyr Thr Ser Pro
201      370                  375                  380
203 agg ttc ctt cca cca acc aag ata gac aat tgc aag att aag gat gcc     1200
204 Arg Phe Leu Pro Pro Thr Lys Ile Asp Asn Cys Lys Ile Lys Asp Ala
205 385               390                  395                  400
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207 ata att tct cat gga tgt ttc ttg cga gat tgc tct gtg gaa cac tcc   1248
208 Ile Ile Ser His Gly Cys Phe Leu Arg Asp Cys Ser Val Glu His Ser
209   405   410   415
211 ata gtg ggt gaa aga tca cgc tta gac tgt ggt gtt gaa ctg aag gat   1296
212 Ile Val Gly Glu Arg Ser Arg Leu Asp Cys Gly Val Glu Leu Lys Asp
213   420   425   430
215 act ttc atg atg gga gca gac tac tac caa aca gaa tct gag att gcc   1344
216 Thr Phe Met Met Gly Ala Asp Tyr Tyr Gln Thr Glu Ser Glu Ile Ala
217   435   440   445
219 tcc ctg tta gca gag ggg aaa gta ccg att ggg att ggg gaa aat aca   1392
220 Ser Leu Leu Ala Glu Gly Lys Val Pro Ile Gly Ile Gly Glu Asn Thr
221   450   455   460
223 aaa ata agg aaa tgt atc att gac aag aac gca aag ata gga aaa aat   1440
224 Lys Ile Arg Lys Cys Ile Ile Asp Lys Asn Ala Lys Ile Gly Lys Asn
225 465   470   475   480
227 gtt tca atc att aat aaa gat ggt gtt caa gag gca gac cga cca gag   1488
228 Val Ser Ile Ile Asn Lys Asp Gly Val Gln Glu Ala Asp Arg Pro Glu
229   485   490   495
231 gaa gga ttc tac ata cga tca ggg ata acc att ata tca gag aaa gcc   1536
232 Glu Gly Phe Tyr Ile Arg Ser Gly Ile Thr Ile Ile Ser Glu Lys Ala
233   500   505   510
235 aca att aga gat gga aca gtt ata tga   1563
236 Thr Ile Arg Asp Gly Thr Val Ile
237   515   520
240 <210> SEQ ID NO: 10
241 <211> LENGTH: 520
242 <212> TYPE: PRT
243 <213> ORGANISM: Lycopersicon hirsutum
245 <400> SEQUENCE: 10
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247 1   5   10   15
249 Asn Gly Glu Lys Glu Ile Phe Gly Glu Lys Met Arg Gly Ser Leu Asn
250   20   25   30
252 Asn Asn Leu Arg Ile Asn Gln Leu Ser Lys Ser Leu Lys Leu Glu Lys
253   35   40   45
255 Lys Glu Lys Lys Ile Lys Pro Gly Val Ala Tyr Ser Val Ile Thr Thr
256   50   55   60
258 Glu Asn Asp Thr Glu Thr Val Phe Val Asp Met Pro Arg Leu Glu Arg
259 65   70   75   80
261 Arg Arg Ala Asn Pro Lys Asp Val Ala Ala Val Ile Leu Gly Gly Gly
262   85   90   95
264 Glu Gly Thr Lys Leu Phe Pro Leu Thr Ser Arg Thr Ala Thr Pro Ala
265   100   105   110
267 Val Pro Val Gly Gly Cys Tyr Arg Leu Ile Asp Ile Pro Met Ser Asn
268   115   120   125
270 Cys Ile Asn Ser Ala Ile Asn Lys Ile Phe Val Leu Thr Gln Tyr Asn
271   130   135   140
273 Ser Ala Ala Leu Asn Arg His Ile Ala Arg Thr Tyr Phe Gly Asn Gly
274 145   150   155   160

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276 Val Ser Phe Gly Asp Gly Phe Val Glu Val Leu Ala Ala Thr Gln Thr
277              165             170             175
279 Pro Gly Glu Ala Gly Lys Lys Trp Phe Gln Gly Thr Ala Asp Ala Val
280              180             185             190
282 Arg Lys Phe Ile Trp Val Phe Glu Asp Ala Lys Asn Lys Asn Ile Glu
283          195             200             205
285 Asn Ile Leu Val Leu Ser Gly Asp His Leu Tyr Arg Met Asp Tyr Met
286          210             215             220
288 Glu Leu Val Gln Asn His Ile Asp Arg Asn Ala Asp Ile Thr Leu Ser
289 225              230             235             240
291 Cys Ala Pro Ala Glu Asp Ser Arg Ala Ser Asp Phe Gly Leu Val Lys
292              245             250             255
294 Ile Asp Ser Arg Gly Arg Val Val Gln Phe Ala Glu Lys Pro Lys Gly
295              260             265             270
297 Phe Glu Leu Lys Ala Met Gln Val Asp Thr Thr Leu Val Gly Leu Ser
298          275             280             285
300 Pro Gln Asp Ala Lys Lys Ser Pro Tyr Ile Ala Ser Met Gly Val Tyr
301      290             295             300
303 Val Phe Lys Thr Asp Val Leu Leu Lys Leu Leu Lys Trp Ser Tyr Pro
304 305              310             315             320
306 Thr Ser Asn Asp Phe Gly Ser Glu Ile Ile Pro Ala Ala Ile Asp Asp
307              325             330             335
309 Tyr Asn Val Gln Ala Tyr Ile Phe Lys Asp Tyr Trp Glu Asp Ile Gly
310              340             345             350
312 Thr Ile Lys Ser Phe Tyr Asn Ala Ser Leu Ala Leu Thr Gln Glu Phe
313          355             360             365
315 Pro Glu Phe Gln Phe Tyr Asp Pro Lys Thr Pro Phe Tyr Thr Ser Pro
316      370             375             380
318 Arg Phe Leu Pro Pro Thr Lys Ile Asp Asn Cys Lys Ile Lys Asp Ala
319 385              390             395             400
321 Ile Ile Ser His Gly Cys Phe Leu Arg Asp Cys Ser Val Glu His Ser
322              405             410             415
324 Ile Val Gly Glu Arg Ser Arg Leu Asp Cys Gly Val Glu Leu Lys Asp
325              420             425             430
327 Thr Phe Met Met Gly Ala Asp Tyr Tyr Gln Thr Glu Ser Glu Ile Ala
328          435             440             445
330 Ser Leu Leu Ala Glu Gly Lys Val Pro Ile Gly Ile Gly Glu Asn Thr
331      450             455             460
333 Lys Ile Arg Lys Cys Ile Ile Asp Lys Asn Ala Lys Ile Gly Lys Asn
334 465              470             475             480
336 Val Ser Ile Ile Asn Lys Asp Gly Val Gln Glu Ala Asp Arg Pro Glu
337              485             490             495
339 Glu Gly Phe Tyr Ile Arg Ser Gly Ile Thr Ile Ile Ser Glu Lys Ala
340          500             505             510
342 Thr Ile Arg Asp Gly Thr Val Ile
343          515             520
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VERIFICATION SUMMARY   DATE: 07/15/2001
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L:13 M:271 C: Current Filing Date differs, Replaced Current Filing Date